#6
6-7-02

Serial Number: 10/080,960

CRF Processing Date: 6-7-02
Edited by: M. SPENCER
Verified by: _____ (STIC sta

ENTERED
see page 6

- [ ] Changed a file from non-ASCII to ASCII

- [ ] Changed the margins in cases where the sequence text was "wrapped" down to the next line.

- [ ] Edited a format error in the Current Application Data section, specifically _____

- [ ] Edited the Current Application Data section with the actual current number. The number inputted by the applicant was [ ] the prior application data; or [ ] other _____ .

- [ ] Added the mandatory heading and subheadings for "Current Application Data".

- [ ] Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

- [ ] Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

- [ ] Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

- [ ] Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

- [ ] Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

- [ ] Inserted colons after headings/subheadings. Headings edited included: _____

- [ ] Deleted extra, invalid, headings used by an applicant, specifically: _____

- [x] Deleted: [x] non-ASCII "garbage" at the beginning/end of files; [ ] secretary initials/filename at end of file; [ ] page numbers throughout text; [ ] other invalid text, such as _____

- [ ] Inserted mandatory headings, specifically: _____

- [ ] Corrected an obvious error in the response, specifically: _____

- [ ] Edited identifiers where upper case is used but lower case is required, or vice versa.

- [ ] Corrected an error in the Number of Sequences field, specifically: _____

- [ ] A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

- [ ] Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

- [ ] Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95
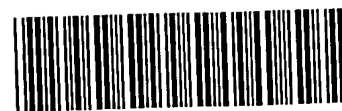
RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/080,960

DATE: 06/07/2002
TIME: 10:50:59

Input Set : N:\jumbos\10080960\PTOMS.txt
Output Set: N:\CRF3\06072002\J080960.raw

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 4 <110> APPLICANT: Millennium Pharmaceuticals, Inc.
 5        Glucksmann, Maria
 6        Meyers, Rachel
 8 <120> TITLE OF INVENTION: 80090, 52874,52880,63497, AND 33425
 9        METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES THEREOF
12 <130> FILE REFERENCE: 38155-20044.00
14 <140> CURRENT APPLICATION NUMBER: US 10/080,960
15 <141> CURRENT FILING DATE: 2001-10-19
17 <150> PRIOR APPLICATION NUMBER: US 60/242,040
18 <151> PRIOR FILING DATE: 2000-10-20
20 <150> PRIOR APPLICATION NUMBER: US 60/242,038
21 <151> PRIOR FILING DATE: 2000-10-20
23 <150> PRIOR APPLICATION NUMBER: US 60/241,992
24 <151> PRIOR FILING DATE: 2000-10-20
26 <150> PRIOR APPLICATION NUMBER: US 60/242,637
27 <151> PRIOR FILING DATE: 2000-10-23
29 <160> NUMBER OF SEQ ID NOS: 37
31 <170> SOFTWARE: FastSEQ for Windows Version 4.0
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 1669
35 <212> TYPE: DNA
36 <213> ORGANISM: Homo sapiens
38 <220> FEATURE:
39 <221> NAME/KEY: CDS
40 <222> LOCATION: (163)...(1623)
42 <400> SEQUENCE: 1
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44 taaagccaat ataatttctt actccttctg gagtgctgct tggctttcac tcagtggttt   120
45 tttttttttt cttttttggc cttggatacc gttgagaatc ta atg aaa gtc acg      174
                                                  Met Lys Val Thr
46                                                   1
47
49 ggc cct ccc cag gga gtt aca gac tcc atg caa tgc ttc aat gat cag      222
50 Gly Pro Pro Gln Gly Val Thr Asp Ser Met Gln Cys Phe Asn Asp Gln
51  5                  10                  15                  20
53 tgg cct tta tct aac acc agg agc agc gag cac ata aaa gag gtc atg      270
54 Trp Pro Leu Ser Asn Thr Arg Ser Ser Glu His Ile Lys Glu Val Met
55                  25                  30                  35
57 gtt gag ctg ggg aag ttt gaa agg aag gag ttt aaa agt tcc agt ttg      318
58 Val Glu Leu Gly Lys Phe Glu Arg Lys Glu Phe Lys Ser Ser Ser Leu
59                  40                  45                  50
61 caa gat gga cat aca aaa atg gag gaa gca cct acg cat ctt aat tca      366
62 Gln Asp Gly His Thr Lys Met Glu Glu Ala Pro Thr His Leu Asn Ser
63                  55                  60                  65
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 65 ttt ctt aag aaa gaa gga ttg acc ttc aac agg aaa aga aaa tgg gaa      414
 66 Phe Leu Lys Lys Glu Gly Leu Thr Phe Asn Arg Lys Arg Lys Trp Glu
 67      70              75              80
 69 ttg gac agc tac ccc att atg ctc tgg tgg tcc ccg ctg acg ggg gag      462
 70 Leu Asp Ser Tyr Pro Ile Met Leu Trp Trp Ser Pro Leu Thr Gly Glu
 71 85              90              95              100
 73 act ggg agg tta ggc caa tgt gga gca gat gct tgt ttc ttc acc atc      510
 74 Thr Gly Arg Leu Gly Gln Cys Gly Ala Asp Ala Cys Phe Phe Thr Ile
 75              105             110             115
 77 aac cgg acc tac ctc cat cat cac atg acc aaa gca ttc ctc ttc tat      558
 78 Asn Arg Thr Tyr Leu His His His Met Thr Lys Ala Phe Leu Phe Tyr
 79              120             125             130
 81 ggt act gac ttt aac ata gat agc tta cct ctg cct cgg aaa gcc cat      606
 82 Gly Thr Asp Phe Asn Ile Asp Ser Leu Pro Leu Pro Arg Lys Ala His
 83          135             140             145
 85 cat gac tgg gct gtt ttt cat gaa gag tcc ccg aaa aac aat tat aag      654
 86 His Asp Trp Ala Val Phe His Glu Glu Ser Pro Lys Asn Asn Tyr Lys
 87      150             155             160
 89 ctc ttt cat aaa cca gtg att acc ttg ttc aac tac act gcc acg ttc      702
 90 Leu Phe His Lys Pro Val Ile Thr Leu Phe Asn Tyr Thr Ala Thr Phe
 91 165             170             175             180
 93 agc agg cat tcc cac ttg cca cta act acc caa tac ttg gag agc att      750
 94 Ser Arg His Ser His Leu Pro Leu Thr Thr Gln Tyr Leu Glu Ser Ile
 95              185             190             195
 97 gaa gtc ctg aag tca ctc cga tac cta gtt cct ttg cag tcc aaa aac      798
 98 Glu Val Leu Lys Ser Leu Arg Tyr Leu Val Pro Leu Gln Ser Lys Asn
 99          200             205             210
101 aag ctt aga aaa aga ctt gct ccg ctg gtg tat gta cag tca gac tgt      846
102 Lys Leu Arg Lys Arg Leu Ala Pro Leu Val Tyr Val Gln Ser Asp Cys
103          215             220             225
105 gac cca cca tca gac agg gac agc tat gtt cgc gag ctg atg act tac      894
106 Asp Pro Pro Ser Asp Arg Asp Ser Tyr Val Arg Glu Leu Met Thr Tyr
107      230             235             240
109 atc gag gtc gat tcc tat ggt gaa tgt tta cga aac aaa gac ctc cct      942
110 Ile Glu Val Asp Ser Tyr Gly Glu Cys Leu Arg Asn Lys Asp Leu Pro
111 245             250             255             260
113 cag cag ctg aaa aat cca gcc tct atg gat gcc gat ggc ttt tat agg      990
114 Gln Gln Leu Lys Asn Pro Ala Ser Met Asp Ala Asp Gly Phe Tyr Arg
115              265             270             275
117 atc att gca cag tat aag ttt atc cta gct ttt gag aat gca gtt tgt     1038
118 Ile Ile Ala Gln Tyr Lys Phe Ile Leu Ala Phe Glu Asn Ala Val Cys
119          280             285             290
121 gat gac tac atc act gag aag ttc tgg agg cca ctg aaa ctg ggg gta     1086
122 Asp Asp Tyr Ile Thr Glu Lys Phe Trp Arg Pro Leu Lys Leu Gly Val
123          295             300             305
125 gtc cct gta tat tac gga tcc ccc agc atc aca gac tgg ctt cca agt     1134
126 Val Pro Val Tyr Tyr Gly Ser Pro Ser Ile Thr Asp Trp Leu Pro Ser
127      310             315             320
129 aac aaa agt gct att ctt gta tca gaa ttt tct cac ccc agg gaa ctg     1182
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130 Asn Lys Ser Ala Ile Leu Val Ser Glu Phe Ser His Pro Arg Glu Leu
131 325                 330             335             340
133 gca agt tac atc aga cga ctg gat tct gat gac aga ttg tat gag gcc      1230
134 Ala Ser Tyr Ile Arg Arg Leu Asp Ser Asp Asp Arg Leu Tyr Glu Ala
135                 345             350             355
137 tat gta gaa tgg aag ctg aag ggt gag atc tct aac cag cga ctt ctg      1278
138 Tyr Val Glu Trp Lys Leu Lys Gly Glu Ile Ser Asn Gln Arg Leu Leu
139                 360             365             370
141 aca gct ctc agg gaa cgg aaa tgg gga gtg caa gac gtc aac cag gac      1326
142 Thr Ala Leu Arg Glu Arg Lys Trp Gly Val Gln Asp Val Asn Gln Asp
143             375             380             385
145 aat tac atc gat gca ttt gag tgt atg gtg tgc acc aag gtg tgg gct      1374
146 Asn Tyr Ile Asp Ala Phe Glu Cys Met Val Cys Thr Lys Val Trp Ala
147             390             395             400
149 aat atc agg ctt cag gaa aag ggc tta cca ccc aaa aga tgg gag gca      1422
150 Asn Ile Arg Leu Gln Glu Lys Gly Leu Pro Pro Lys Arg Trp Glu Ala
151 405                 410             415             420
153 gaa gat acc cac ctg agt tgc cca gag ccc aca gtg ttt gct ttc tca      1470
154 Glu Asp Thr His Leu Ser Cys Pro Glu Pro Thr Val Phe Ala Phe Ser
155             425             430             435
157 cca ctc cgg act cca cct ttg agc tct ttg cga gag atg tgg att tcc      1518
158 Pro Leu Arg Thr Pro Pro Leu Ser Ser Leu Arg Glu Met Trp Ile Ser
159             440             445             450
161 agc ttt gaa caa tcc aag aaa gaa gcc cag gca cta agg tgg ctg gtt      1566
162 Ser Phe Glu Gln Ser Lys Lys Glu Ala Gln Ala Leu Arg Trp Leu Val
163             455             460             465
165 gat agg aat caa aac ttt tca tct caa gag ttt tgg ggc cta gta ttc      1614
166 Asp Arg Asn Gln Asn Phe Ser Ser Gln Glu Phe Trp Gly Leu Val Phe
167             470             475             480
169 aag gac tga tttcaaaaat gatcagaatg aaacagaaaa aaaaaaaaaa            1663
170 Lys Asp  *
171 485
173 aaaaaa                                                               1669
175 <210> SEQ ID NO: 2
176 <211> LENGTH: 486
177 <212> TYPE: PRT
178 <213> ORGANISM: Homo sapiens
180 <400> SEQUENCE: 2
181 Met Lys Val Thr Gly Pro Pro Gln Gly Val Thr Asp Ser Met Gln Cys
182 1               5               10              15
183 Phe Asn Asp Gln Trp Pro Leu Ser Asn Thr Arg Ser Ser Glu His Ile
184             20              25              30
185 Lys Glu Val Met Val Glu Leu Gly Lys Phe Glu Arg Lys Glu Phe Lys
186             35              40              45
187 Ser Ser Ser Leu Gln Asp Gly His Thr Lys Met Glu Glu Ala Pro Thr
188     50              55              60
189 His Leu Asn Ser Phe Leu Lys Lys Glu Gly Leu Thr Phe Asn Arg Lys
190 65              70              75              80
191 Arg Lys Trp Glu Leu Asp Ser Tyr Pro Ile Met Leu Trp Trp Ser Pro
```

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192                    85                  90                  95
193 Leu Thr Gly Glu Thr Gly Arg Leu Gly Gln Cys Gly Ala Asp Ala Cys
194              100                 105                 110
195 Phe Phe Thr Ile Asn Arg Thr Tyr Leu His His His Met Thr Lys Ala
196              115                 120                 125
197 Phe Leu Phe Tyr Gly Thr Asp Phe Asn Ile Asp Ser Leu Pro Leu Pro
198      130                 135                 140
199 Arg Lys Ala His His Asp Trp Ala Val Phe His Glu Glu Ser Pro Lys
200 145                 150                 155                 160
201 Asn Asn Tyr Lys Leu Phe His Lys Pro Val Ile Thr Leu Phe Asn Tyr
202              165                 170                 175
203 Thr Ala Thr Phe Ser Arg His Ser His Leu Pro Leu Thr Thr Gln Tyr
204              180                 185                 190
205 Leu Glu Ser Ile Glu Val Leu Lys Ser Leu Arg Tyr Leu Val Pro Leu
206              195                 200                 205
207 Gln Ser Lys Asn Lys Leu Arg Lys Arg Leu Ala Pro Leu Val Tyr Val
208      210                 215                 220
209 Gln Ser Asp Cys Asp Pro Pro Ser Asp Arg Asp Ser Tyr Val Arg Glu
210 225                 230                 235                 240
211 Leu Met Thr Tyr Ile Glu Val Asp Ser Tyr Gly Glu Cys Leu Arg Asn
212              245                 250                 255
213 Lys Asp Leu Pro Gln Gln Leu Lys Asn Pro Ala Ser Met Asp Ala Asp
214      260                 265                 270
215 Gly Phe Tyr Arg Ile Ile Ala Gln Tyr Lys Phe Ile Leu Ala Phe Glu
216      275                 280                 285
217 Asn Ala Val Cys Asp Asp Tyr Ile Thr Glu Lys Phe Trp Arg Pro Leu
218      290                 295                 300
219 Lys Leu Gly Val Val Pro Val Tyr Tyr Gly Ser Pro Ser Ile Thr Asp
220 305                 310                 315                 320
221 Trp Leu Pro Ser Asn Lys Ser Ala Ile Leu Val Ser Glu Phe Ser His
222              325                 330                 335
223 Pro Arg Glu Leu Ala Ser Tyr Ile Arg Arg Leu Asp Ser Asp Asp Arg
224      340                 345                 350
225 Leu Tyr Glu Ala Tyr Val Glu Trp Lys Leu Lys Gly Glu Ile Ser Asn
226      355                 360                 365
227 Gln Arg Leu Leu Thr Ala Leu Arg Glu Arg Lys Trp Gly Val Gln Asp
228      370                 375                 380
229 Val Asn Gln Asp Asn Tyr Ile Asp Ala Phe Glu Cys Met Val Cys Thr
230 385                 390                 395                 400
231 Lys Val Trp Ala Asn Ile Arg Leu Gln Glu Lys Gly Leu Pro Pro Lys
232              405                 410                 415
233 Arg Trp Glu Ala Glu Asp Thr His Leu Ser Cys Pro Glu Pro Thr Val
234              420                 425                 430
235 Phe Ala Phe Ser Pro Leu Arg Thr Pro Pro Leu Ser Ser Leu Arg Glu
236      435                 440                 445
237 Met Trp Ile Ser Ser Phe Glu Gln Ser Lys Lys Glu Ala Gln Ala Leu
238      450                 455                 460
239 Arg Trp Leu Val Asp Arg Asn Gln Asn Phe Ser Ser Gln Glu Phe Trp
240 465                 470                 475                 480
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241 Gly Leu Val Phe Lys Asp
242                     485
244 <210> SEQ ID NO: 3
245 <211> LENGTH: 1461
246 <212> TYPE: DNA
247 <213> ORGANISM: Homo sapiens
249 <400> SEQUENCE: 3
250 atgaaagtca cgggccctcc ccagggagtt acagactcca tgcaatgctt caatgatcag      60
251 tggcctttat ctaacaccag gagcagcgag cacataaaag aggtcatggt tgagctgggg     120
252 aagtttgaaa ggaaggagtt taaaagttcc agtttgcaag atggacatac aaaaatggag     180
253 gaagcaccta cgcatcttaa ttcatttctt aagaaagaag gattgacctt caacaggaaa     240
254 agaaaatggg aattggacag ctaccccatt atgctctggt ggtccccgct gacggggag     300
255 actgggaggt taggccaatg tggagcagat gcttgtttct tcaccatcaa ccggacctac     360
256 ctccatcatc acatgaccaa agcattcctc ttctatggta ctgactttaa catagatagc     420
257 ttacctctgc ctcggaaagc ccatcatgac tgggctgttt ttcatgaaga gtccccgaaa     480
258 aacaattata agctctttca taaaccagtg attaccttgt tcaactacac tgccacgttc     540
259 agcaggcatt cccacttgcc actaactacc caatacttgg agagcattga agtcctgaag     600
260 tcactccgat acctagttcc tttgcagtcc aaaaacaagc ttagaaaaag acttgctccg     660
261 ctggtgtatg tacagtcaga ctgtgaccca ccatcagaca gggacagcta tgttcgcgag     720
262 ctgatgactt acatcgaggt cgattcctat ggtgaatgtt tacgaaacaa agacctccct     780
263 cagcagctga aaaatccagc ctctatggat gccgatggct tttataggat cattgcacag     840
264 tataagttta tcctagcttt tgagaatgca gtttgtgatg actacatcac tgagaagttc     900
265 tggaggccac tgaaactggg ggtagtccct gtatattacg gatcccccag catcacagac     960
266 tggcttccaa gtaacaaaag tgctattctt gtatcagaat tttctcaccc cagggaactg    1020
267 gcaagttaca tcagacgact ggattctgat gacagattgt atgaggccta tgtagaatgg    1080
268 aagctgaagg gtgagatctc taaccagcga cttctgacag ctctcaggga acggaaatgg    1140
269 ggagtgcaag acgtcaacca ggacaattac atcgatgcat ttgagtgtat ggtgtgcacc    1200
270 aaggtgtggg ctaatatcag gcttcaggaa aagggcttac cacccaaaag atggggaggca    1260
271 gaagataccc acctgagttg cccagagccc acagtgtttg ctttctcacc actccggact    1320
272 ccacctttga gctctttgcg agagatgtgg atttccagct ttgaacaatc caagaaagaa    1380
273 gcccaggcac taaggtggct ggttgatagg aatcaaaact tttcatctca agagtttgg    1440
                                                                       1461
274 ggcctagtat tcaaggactg a
276 <210> SEQ ID NO: 4
277 <211> LENGTH: 1420
278 <212> TYPE: DNA
279 <213> ORGANISM: Homo sapiens
281 <220> FEATURE:
282 <221> NAME/KEY: CDS
283 <222> LOCATION: (32)...(1417)
285 <400> SEQUENCE: 4
286 agctgccttt gcagactcta actccagcag c atg aat gtg tcc ttt gct cac       52
                                         Met Asn Val Ser Phe Ala His
287                                       1                   5
288
290 ctc cac ttt gcc gga ggg tac ctg ccc tct gat tcc cag gac tgg aga     100
291 Leu His Phe Ala Gly Gly Tyr Leu Pro Ser Asp Ser Gln Asp Trp Arg
292         10              15                  20
294 acc atc atc ccg gct ctc ttg gtg gct gtc tgc ctg gtg ggc ttc gtg     148
295 Thr Ile Ile Pro Ala Leu Leu Val Ala Val Cys Leu Val Gly Phe Val
296         25              30                  35
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 06/07/2002
PATENT APPLICATION: US/10/080,960   TIME: 10:51:00

Input Set : N:\jumbos\10080960\PTOMS.txt
Output Set: N:\CRF3\06072002\J080960.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:36; Xaa Pos. 28,29,38,39,74,75
Seq#:37; Xaa Pos. 13,14,15,39,40,47,48

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/080,960

DATE: 06/07/2002
TIME: 10:51:00

Input Set : **N:\jumbos\10080960\PTOMS.txt**
Output Set: **N:\CRF3\06072002\J080960.raw**

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L:1836 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1840 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:36
L:1843 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:16
L:1845 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:32
L:1849 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:64
L:1860 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1864 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:37
L:1865 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:0
L:1869 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:32
```

Does Not Comply
Corrected Diskette Needed

||||||||||||||||||||||||||||||||||||||

OIPE

RAW SEQUENCE LISTING   DATE: 06/03/2002
PATENT APPLICATION: US/10/080,960   TIME: 13:48:06

Input Set : D:\38155-20044.txt
Output Set: N:\CRF3\06032002\J080960.raw

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  4 <110> APPLICANT: Millennium Pharmaceuticals, Inc.
  5         Glucksmann, Maria
  6         Meyers, Rachel
  8 <120> TITLE OF INVENTION: 80090, 52874,52880,63497, AND 33425
  9         METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES THEREOF
 12 <130> FILE REFERENCE: 38155-20044.00
 14 <140> CURRENT APPLICATION NUMBER: US 10/080,960
 15 <141> CURRENT FILING DATE: 2001-10-19
 17 <150> PRIOR APPLICATION NUMBER: US 60/242,040
 18 <151> PRIOR FILING DATE: 2000-10-20
 20 <150> PRIOR APPLICATION NUMBER: US 60/242,038
 21 <151> PRIOR FILING DATE: 2000-10-20
 23 <150> PRIOR APPLICATION NUMBER: US 60/241,992
 24 <151> PRIOR FILING DATE: 2000-10-20
 26 <150> PRIOR APPLICATION NUMBER: US 60/242,637
 27 <151> PRIOR FILING DATE: 2000-10-23
 29 <160> NUMBER OF SEQ ID NOS: 37
 31 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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ERRORED SEQUENCES

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       1852 <210> SEQ ID NO: 37
       1853 <211> LENGTH: 50
       1854 <212> TYPE: PRT
       1855 <213> ORGANISM: Artificial Sequence
       1857 <220> FEATURE:
       1858 <223> OTHER INFORMATION: Consensus amino acid sequence
W--> 1860 <221> NAME/KEY: VARIANT
       1861 <222> LOCATION: (1)...(50)
       1862 <223> OTHER INFORMATION: Xaa = Any Amino Acid
W--> 1864 <400> 37
W--> 1865 Leu Ile Val Met Phe Trp Ala Cys Pro Gly Ala Cys Xaa Xaa Xaa Ser
       1866  1               5                  10                  15
       1867 Ala Cys Lys Ser Thr Ala Leu Ile Met Arg Gly Ser Ala Cys Pro Asn
       1868            20                  25                  30
W--> 1869 Val Ser Thr Ala Cys Pro Xaa Xaa Asp Glu Asn Phe Ala Pro Xaa Xaa
       1870            35                  40                  45
       1871 Ile Tyr
       1872           50
E--> 1874 1
E--> 1877 33
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— remove extra material at end of file

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/080,960

DATE: 06/03/2002
TIME: 13:48:07

Input Set : D:\38155-20044.txt
Output Set: N:\CRF3\06032002\J080960.raw

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L:1836 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1840 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:36
L:1843 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:16
L:1845 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:32
L:1849 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:64
L:1860 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:1864 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:37
L:1865 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:0
L:1869 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:32
L:1874 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:37
M:332 Repeated in SeqNo=37
```